Non-tuberculous Mycobacteria Isolated from New Zealand Soil Environments

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Abstract

There is little information on the diversity of non-tuberculous mycobacteria (NTM) in New Zealand. This project has shown that diverse mycobacteria can be isolated from forest, pastoral and urban environments through the combined use of specialised decontamination techniques and selective media. *Mycobacterium avium-intracellulare* complex (MAIC) was the most commonly isolated mycobacteria (40%) followed by *M. montefiorense/M. triplex* (20%). This is the first known isolation of *M. montefiorense/M. triplex* from soils in New Zealand. The greatest numbers of mycobacteria were isolated from peat-rich pastoral soils, followed by urban dust/organic matter and native forest soils. The majority of mycobacteria isolated were slow-growing. The greatest numbers of isolates that were unable to be speciated further than *Mycobacterium* species using 16S rDNA sequencing (i.e. likely to be new species) were isolated from native forest soils.

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Chapter 1 Introduction

Worldwide, the incidence of environmental mycobacterial infections is increasing but there are limited data on the diversity of mycobacteria isolated from the environment. Often the studies available have focussed on a particular species associated with human disease rather than on overall diversity. Without a baseline knowledge of species diversity it is difficult to assess changes within the mycobacterial population and whether a previously uncommon isolate may now cause disease due to a change in habitat. Unlike tuberculosis, infection due to non-tuberculous mycobacteria is not a notifiable disease. Therefore, limited data on the number, type and epidemiology of non-tuberculous mycobacterial infections in New Zealand are available. It is believed that *Mycobacterium avium* complex (MAC) is the most common cause of non-tuberculous mycobacterial infections in New Zealand and Australia. It is a well known fact that the environment is the primary source of MAC infection (Falkinham 1996).

Exposure of MAC isolates to macrolides, antibiotics commonly used to treat MAC infections, has been identified as a major factor in the development of antimicrobial resistance (Stormer *et al.* 1989; Yago *et al.* 1995). Exposure to sub-inhibitory levels of these antibiotics found in the environment may also contribute to this resistance (Kummerer 2004). There are no local data available on the antimicrobial susceptibility of MAC isolates from the environment. Without available data it is difficult to assess if human impact (i.e., agriculture or urbanisation) has had any effect on the susceptibility of wild type MAC to macrolide antibiotics and if drug resistant MAC strains exist in the New Zealand environment.

The aim of this project was to develop improved techniques to isolate environmental mycobacteria and to compare the diversity of mycobacterial species from different New Zealand soil environments using genotypic methods for identification. The susceptibility of MAC isolates to macrolides was also assessed to investigate whether specific environments harbour isolates with increased resistance to macrolide antibiotics.

Knowledge of mycobacterial diversity and antimicrobial susceptibility may provide insights into the indigenous mycobacterial populations in New Zealand soil environments. Data on existing mycobacterial populations, their environmental niche and susceptibility to antibiotics can be used to enhance our ability to predict and prevent conditions that lead to infections. These data may be used to further understand the effect of human impact on the susceptibility and epidemiology of non-tuberculous mycobacteria.